<u>**Amendments to the Claims**</u>

This listing of claims will replace all prior versions, and listings, of claims in the application.

<u>**Listing of Claims**</u>

Claim 1 (currently amended): A method of predicting a scaffold of a protein comprising a query sequence, wherein said method uses a database which contains environmental information on the side chain of each amino acid residue contained in the amino acid sequence of each reference protein whose three-dimensional structure is known or predictable, wherein the amino acid sequence of each of the reference proteins is divided into two or more <u>core</u> segment sequences comprising two or more contiguous amino acid residues based on the characteristics of the three-dimensional structure of the reference protein and wherein said method comprises:

conducting matching based on the environmental information on each amino acid residue of each of the two or more <u>core</u> segment sequences of the reference protein and hydrophobicity or hydrophilicity property of the side chain of each amino acid residue of the query sequence, and

choosing at least one template protein among the reference proteins that has ~~high~~ <u>highest</u> similarity in three-dimensional structure to the protein comprising the query sequence and predicting the scaffold of the protein comprising a query sequence.

Claim 2 (canceled)

Claim 3 (previously presented): The method according to claim 1, wherein the amino acid sequence of each of the reference proteins is divided into one or more core segment sequences which are predetermined to form a hydrophobic core, and into one or more sub segment sequences which are not predetermined to form a hydrophobic core.

Claim 4 (previously presented): The method according to claim 1, wherein the matching is conducted based on the information on degree of burial into the inside of the protein of the side chain of each amino acid residue in the reference protein, or degree of exposure to the protein surface of the side chain of each amino acid residue in the reference protein, together with the properties of hydrophobicity or hydrophilicity of each amino acid residue in the query sequence.

Claim 5 (previously presented): The method according to claim 1, wherein the matching is performed by sliding the two or more core segment sequences of the reference protein on the query sequence without consideration of any gaps except those at one end or both ends of the core segment sequence.

Claim 6 (previously presented): The method according to claim 5, wherein the gap is a deletion or addition of one or more amino acid residues.

Claim 7 (currently amended): The method according to claim 1, wherein the matching comprises: matching by sliding the two or more core segment sequences of the reference protein on the query sequence, optionally considering gaps at one end or both ends of the core segment sequences, wherein the core segment sequences are placed in the order of appearance on the amino acid sequence of the reference protein; and, sliding

one or more sub segment sequences on the query sequence, optionally considering one or more gaps.

Claim 8 (previously presented): The method according to claim 1, wherein an optimum matching is selected based on calculated scores obtained from the environmental information on the side chains of the amino acid residues of the reference protein and the hydrophobicity parameters of the corresponding amino acid residues on the query sequence.

Claim 9 (previously presented): The method according to claim 8, which further comprises normalizing the above scores by using a self matching score for the reference protein.

Claim 10 (previously presented): The method according to claim 1, which further comprises constructing the three-dimensional structure of the protein comprising the query sequence.

Claims 11-20 (canceled)